

## SEQUENCE LISTING

<110> BURTON, Paul B. J.  
DEISHER, Theresa A.

<120> COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE

<130> 3432-B

<140> -to be assigned-

<141> 2003-08-21

<150> --to be assigned--

<151> 2003-08-12

<150> 60/406,418

<151> 2002-08-28

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<170> PatentIn version 3.2

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Glu	Glu	Gly	Gly	Ala	Ala	Val	Ala	Lys	Leu	Glu	Pro	His	Leu	Gln	Pro
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Glu	Glu	Gly	Ala	Leu	Val	Ala	Ala	Val	Glu	Pro	Gly	Pro	Leu	Ala	Asp
		675					680					685			

Gly Ala Ala Val Arg Leu Ala Leu Ala Gly Glu Gly Glu Ala Cys Pro  
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 Leu Leu Gly Ser Pro Gly Ala Gly Arg Asn Ser Val Leu Phe Leu Pro  
 705 710 715 720  
 Val Asp Pro Glu Asp Ser Pro Leu Gly Ser Ser Thr Pro Met Ala Ser  
 725 730 735  
 Pro Asp Leu Leu Pro Glu Asp Val Arg Glu His Leu Glu Gly Leu Met  
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 Leu Ser Leu Phe Glu Gln Ser Leu Ser Cys Gln Ala Gln Gly Gly Cys  
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 Ser Arg Pro Ala Met Val Leu Thr Asp Pro His Thr Pro Tyr Glu Glu  
 770 775 780  
 Glu Gln Arg Gln Ser Val Gln Ser Asp Gln Gly Tyr Ile Ser Arg Ser  
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 Ser Pro Gln Pro Pro Glu Gly Leu Thr Glu Met Glu Glu Glu Glu Glu  
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 Glu Glu Gln Asp Pro Gly Lys Pro Ala Leu Pro Leu Ser Pro Glu Asp  
 820 825 830  
 Leu Glu Ser Leu Arg Ser Leu Gln Arg Gln Leu Leu Phe Arg Gln Leu  
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 1 5 10 15  
 agc act gca gaa tct tgt act tca cgt ccc cac att act gtg gtt gaa 96  
 Ser Thr Ala Glu Ser Cys Thr Ser Arg Pro His Ile Thr Val Val Glu  
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 ggg gaa cct ttc tat ctg aaa cat tgc tcg tgt tca ctt gca cat gag 144  
 Gly Glu Pro Phe Tyr Leu Lys His Cys Ser Cys Ser Leu Ala His Glu  
 35 40 45

att gaa aca acc acc aaa agc tgg tac aaa agc agt gga tca cag gaa Ile Glu Thr Thr Thr Lys Ser Trp Tyr Lys Ser Ser Gly Ser Gln Glu 50 55 60	192
cat gtg gag ctg aac cca agg agt tcc tcg aga att gct ttg cat gat His Val Glu Leu Asn Pro Arg Ser Ser Ser Arg Ile Ala Leu His Asp 65 70 75 80	240
tgt gtt ttg gag ttt tgg cca gtt gag ttg aat gac aca gga tct tac Cys Val Leu Glu Phe Trp Pro Val Glu Leu Asn Asp Thr Gly Ser Tyr 85 90 95	288
ttt ttc caa atg aaa aat tat act cag aaa tgg aaa tta aat gtc atc Phe Phe Gln Met Lys Asn Tyr Thr Gln Lys Trp Lys Leu Asn Val Ile 100 105 110	336
aga aga aat aaa cac agc tgt ttc act gaa aga caa gta act agt aaa Arg Arg Asn Lys His Ser Cys Phe Thr Glu Arg Gln Val Thr Ser Lys 115 120 125	384
att gtg gaa gtt aaa aaa ttt ttt cag ata acc tgt gaa aac agt tac Ile Val Glu Val Lys Lys Phe Phe Gln Ile Thr Cys Glu Asn Ser Tyr 130 135 140	432
tat caa aca ctg gtc aac agc aca tca ttg tat aag aac tgt aaa aag Tyr Gln Thr Leu Val Asn Ser Thr Ser Leu Tyr Lys Asn Cys Lys Lys 145 150 155 160	480
cta cta ctg gag aac aat aaa aac cca acg ata aag aag aac gcc gag Leu Leu Leu Glu Asn Asn Lys Asn Pro Thr Ile Lys Lys Asn Ala Glu 165 170 175	528
ttt gaa gat cag ggg tat tac tcc tgc gtg cat ttc ctt cat cat aat Phe Glu Asp Gln Gly Tyr Tyr Ser Cys Val His Phe Leu His His Asn 180 185 190	576
gga aaa cta ttt aat atc acc aaa acc ttc aat ata aca ata gtg gaa Gly Lys Leu Phe Asn Ile Thr Lys Thr Phe Asn Ile Thr Ile Val Glu 195 200 205	624
gat cgc agt aat ata gtt ccg gtt ctt ctt gga cca aag ctt aac cat Asp Arg Ser Asn Ile Val Pro Val Leu Leu Gly Pro Lys Leu Asn His 210 215 220	672
gtt gca gtg gaa tta gga aaa aac gta agg ctc aac tgc tct gct ttg Val Ala Val Glu Leu Gly Lys Asn Val Arg Leu Asn Cys Ser Ala Leu 225 230 235 240	720
ctg aat gaa gag gat gta att tat tgg atg ttt ggg gaa gaa aat gga Leu Asn Glu Glu Asp Val Ile Tyr Trp Met Phe Gly Glu Glu Asn Gly 245 250 255	768
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gaa agc aat cta aat gtt tta tat aat tgc act gtg gcc agc acg gga	912

Glu Ser Asn Leu Asn Val Leu Tyr Asn Cys Thr Val Ala Ser Thr Gly	
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ggc aca gac acc aaa agc ttc atc ttg gtg aga aaa gca gac atg gct	960
Gly Thr Asp Thr Lys Ser Phe Ile Leu Val Arg Lys Ala Asp Met Ala	
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Asp Ile Pro Gly His Val Phe Thr Arg Gly Met Ile Ile Ala Val Leu	
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Ile Leu Val Ala Val Val Cys Leu Val Thr Val Cys Val Ile Tyr Arg	
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Val Asp Leu Val Leu Phe Tyr Arg His Leu Thr Arg Arg Asp Glu Thr	
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Leu Thr Asp Gly Lys Thr Tyr Asp Ala Phe Val Ser Tyr Leu Lys Glu	
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Cys Arg Pro Glu Asn Gly Glu Glu His Thr Phe Ala Val Glu Ile Leu	
385 390 395 400	
ccc agg gtg ttg gag aaa cat ttt ggg tat aag tta tgc ata ttt gaa	1248
Pro Arg Val Leu Glu Lys His Phe Gly Tyr Lys Leu Cys Ile Phe Glu	
405 410 415	
agg gat gta gtg cct gga gga gct gtt gtt gat gaa atc cac tca ctg	1296
Arg Asp Val Val Pro Gly Gly Ala Val Val Asp Glu Ile His Ser Leu	
420 425 430	
ata gag aaa agc cga aga cta atc att gtc cta agt aaa agt tat atg	1344
Ile Glu Lys Ser Arg Arg Leu Ile Ile Val Leu Ser Lys Ser Tyr Met	
435 440 445	
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Ser Asn Glu Val Arg Tyr Glu Leu Glu Ser Gly Leu His Glu Ala Leu	
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465 470 475 480	
gac ttc aca ttc ttg ccc caa tca cta aag ctt ttg aaa tct cac aga	1488
Asp Phe Thr Phe Leu Pro Gln Ser Leu Lys Leu Leu Lys Ser His Arg	
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gtt ctg aag tgg aag gcc gat aaa tct ctt tct tat aac tca agg ttc	1536
Val Leu Lys Trp Lys Ala Asp Lys Ser Leu Ser Tyr Asn Ser Arg Phe	
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Trp Lys Asn Leu Leu Tyr Leu Met Pro Ala Lys Thr Val Lys Pro Gly	
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 Gly Thr Asp Thr Lys Ser Phe Ile Leu Val Arg Lys Ala Asp Met Ala  
 305 310 315 320  
 Asp Ile Pro Gly His Val Phe Thr Arg Gly Met Ile Ile Ala Val Leu  
 325 330 335  
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 340 345 350  
 Val Asp Leu Val Leu Phe Tyr Arg His Leu Thr Arg Arg Asp Glu Thr  
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 Cys Arg Pro Glu Asn Gly Glu Glu His Thr Phe Ala Val Glu Ile Leu  
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 Ser Asn Glu Val Arg Tyr Glu Leu Glu Ser Gly Leu His Glu Ala Leu  
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 465 470 475 480  
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aggacaacat atgggtgatgg ggaaatcaga agctttgaga ccctctacac ctggatatga      360
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aca atg ctc tgt ttg ggc tgg ata ttt ctt tgg ctt gtt gca gga gag      528
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cga att aaa gga ttt aat att tca ggt tgt tcc aca aaa aaa ctc ctt      576
Arg Ile Lys Gly Phe Asn Ile Ser Gly Cys Ser Thr Lys Lys Leu Leu
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tgg aca tat tct aca agg agt gaa gag gaa ttt gtc tta ttt tgt gat      624
Trp Thr Tyr Ser Thr Arg Ser Glu Glu Glu Phe Val Leu Phe Cys Asp
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tta cca gag cca cag aaa tca cat ttc tgc cac aga aat cga ctc tca      672
Leu Pro Glu Pro Gln Lys Ser His Phe Cys His Arg Asn Arg Leu Ser
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cca aaa caa gtc cct gag cac ctg ccc ttc atg ggt agt aac gac cta      720
Pro Lys Gln Val Pro Glu His Leu Pro Phe Met Gly Ser Asn Asp Leu
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tct gat gtc caa tgg tac caa caa cct tcg aat gga gat cca tta gag      768
Ser Asp Val Gln Trp Tyr Gln Gln Pro Ser Asn Gly Asp Pro Leu Glu
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gac att agg aaa agc tat cct cac atc att cag gac aaa tgt acc ctt      816
Asp Ile Arg Lys Ser Tyr Pro His Ile Ile Gln Asp Lys Cys Thr Leu
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cac ttt ttg acc cca ggg gtg aat aat tct ggg tca tat att tgt aga      864
His Phe Leu Thr Pro Gly Val Asn Asn Ser Gly Ser Tyr Ile Cys Arg
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ccc aag atg att aag agc ccc tat gat gta gcc tgt tgt gtc aag atg      912
Pro Lys Met Ile Lys Ser Pro Tyr Asp Val Ala Cys Cys Val Lys Met
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att tta gaa gtt aag ccc cag aca aat gca tcc tgt gag tat tcc gca      960
Ile Leu Glu Val Lys Pro Gln Thr Asn Ala Ser Cys Glu Tyr Ser Ala
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tca cat aag caa gac cta ctt ctt ggg agc act ggc tct att tct tgc      1008
Ser His Lys Gln Asp Leu Leu Leu Gly Ser Thr Gly Ser Ile Ser Cys
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agc tgc aaa gca cga ttt ggc ttt gaa agg gtc ttt aac cct gtc ata Ser Cys Lys Ala Arg Phe Gly Phe Glu Arg Val Phe Asn Pro Val Ile 275 280 285	1344
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His Leu Ala Leu Ser Leu Phe Pro Asp Val Leu Glu Asn Lys Tyr Gly	
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Tyr Ser Leu Cys Leu Leu Glu Arg Asp Val Ala Pro Gly Gly Val Tyr	
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Ala Ala Val Asn Leu Ala Leu Asp Asp Gln Thr Leu Lys Leu Ile Leu	
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Ile Lys Phe Cys Tyr Phe Gln Glu Pro Glu Ser Leu Pro His Leu Val	
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Lys Lys Ala Leu Arg Val Leu Pro Thr Val Thr Trp Arg Gly Leu Lys	
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Ser Val Pro Pro Asn Ser Arg Phe Trp Ala Lys Met Arg Tyr His Met	
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Pro Val Lys Asn Ser Gln Gly Phe Thr Trp Asn Gln Leu Arg Ile Thr	
560 565 570 575	
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Ser Arg Ile Phe Gln Trp Lys Gly Leu Ser Arg Thr Glu Thr Thr Gly	
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Arg Ser Ser Gln Pro Lys Glu Trp	
595	
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Thr	Tyr	Ser	Thr	Arg	Ser	Glu	Glu	Glu	Phe	Val	Leu	Phe	Cys	Asp	Leu	35	40	45	
Pro	Glu	Pro	Gln	Lys	Ser	His	Phe	Cys	His	Arg	Asn	Arg	Leu	Ser	Pro	50	55	60	
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Asp	Val	Gln	Trp	Tyr	Gln	Gln	Pro	Ser	Asn	Gly	Asp	Pro	Leu	Glu	Asp	85	90	95	
Ile	Arg	Lys	Ser	Tyr	Pro	His	Ile	Ile	Gln	Asp	Lys	Cys	Thr	Leu	His	100	105	110	
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His	Lys	Gln	Asp	Leu	Leu	Leu	Gly	Ser	Thr	Gly	Ser	Ile	Ser	Cys	Pro	165	170	175	
Ser	Leu	Ser	Cys	Gln	Ser	Asp	Ala	Gln	Ser	Pro	Ala	Val	Thr	Trp	Tyr	180	185	190	
Lys	Asn	Gly	Lys	Leu	Leu	Ser	Val	Glu	Arg	Ser	Asn	Arg	Ile	Val	Val	195	200	205	
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Cys	Lys	Ala	Arg	Phe	Gly	Phe	Glu	Arg	Val	Phe	Asn	Pro	Val	Ile	Lys				

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Thr	Leu	Gly	Asp	Lys	Lys	Asp	Phe	Asp	Ala	Phe	Val	Ser	Tyr	Ala	Lys
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Ala	Val	Asn	Leu	Ala	Leu	Asp	Asp	Gln	Thr	Leu	Lys	Leu	Ile	Leu	Ile
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 Met Arg His Asn Trp Thr Pro Asp Leu Ser Pro Leu Trp Val Leu  
 1 5 10 15  
 ctc ctg tgt gcc cac gtc gtc act ctc ctg gtc aga gcc aca cct gtc 158  
 Leu Leu Cys Ala His Val Val Thr Leu Leu Val Arg Ala Thr Pro Val  
 20 25 30  
 tcg cag acc acc aca gct gcc act gcc tca gtt aga agc aca aag gac 206  
 Ser Gln Thr Thr Thr Ala Ala Thr Ala Ser Val Arg Ser Thr Lys Asp  
 35 40 45  
 ccc tgc ccc tcc cag ccc cca gtg ttc cca gca gct aag cag tgt cca 254  
 Pro Cys Pro Ser Gln Pro Pro Val Phe Pro Ala Ala Lys Gln Cys Pro  
 50 55 60  
 gca ttg gaa gtg acc tgg cca gag gtg gaa gtg cca ctg aat gga acg 302  
 Ala Leu Glu Val Thr Trp Pro Glu Val Glu Val Pro Leu Asn Gly Thr  
 65 70 75  
 ctg agc tta tcc tgt gtg gcc tgc agc cgc ttc ccc aac ttc agc atc 350  
 Leu Ser Leu Ser Cys Val Ala Cys Ser Arg Phe Pro Asn Phe Ser Ile  
 80 85 90 95  
 ctc tac tgg ctg ggc aat ggt tcc ttc att gag cac ctc cca ggc cga 398  
 Leu Tyr Trp Leu Gly Asn Gly Ser Phe Ile Glu His Leu Pro Gly Arg  
 100 105 110  
 ctg tgg gag ggg agc acc agc cgg gaa cgt ggg agc aca ggt acg cag 446  
 Leu Trp Glu Gly Ser Thr Ser Arg Glu Arg Gly Ser Thr Gly Thr Gln  
 115 120 125  
 ctg tgc aag gcc ttg gtg ctg gag cag ctg acc cct gcc ctg cac agc 494  
 Leu Cys Lys Ala Leu Val Leu Glu Gln Leu Thr Pro Ala Leu His Ser  
 130 135 140  
 acc aac ttc tcc tgt gtg ctc gtg gac cct gaa cag gtt gtc cag cgt 542  
 Thr Asn Phe Ser Cys Val Leu Val Asp Pro Glu Gln Val Val Gln Arg  
 145 150 155  
 cac gtc gtc ctg gcc cag ctc tgg gct ggg ctg agg gca acc ttg ccc 590  
 His Val Val Leu Ala Gln Leu Trp Ala Gly Leu Arg Ala Thr Leu Pro  
 160 165 170 175  
 ccc acc caa gaagccctgc cctccagcca cagcagtcga cagcagcagg gttaa 644  
 Pro Thr Gln

<210> 10  
 <211> 178  
 <212> PRT  
 <213> Homo sapiens

<400> 10

Met	Arg	His	Asn	Trp	Thr	Pro	Asp	Leu	Ser	Pro	Leu	Trp	Val	Leu	Leu
1			5					10						15	
Leu	Cys	Ala	His	Val	Val	Thr	Leu	Leu	Val	Arg	Ala	Thr	Pro	Val	Ser
			20				25						30		
Gln	Thr	Thr	Thr	Ala	Ala	Thr	Ala	Ser	Val	Arg	Ser	Thr	Lys	Asp	Pro
		35				40						45			
Cys	Pro	Ser	Gln	Pro	Pro	Val	Phe	Pro	Ala	Ala	Lys	Gln	Cys	Pro	Ala
	50					55					60				
Leu	Glu	Val	Thr	Trp	Pro	Glu	Val	Glu	Val	Pro	Leu	Asn	Gly	Thr	Leu
65					70					75					80
Ser	Leu	Ser	Cys	Val	Ala	Cys	Ser	Arg	Phe	Pro	Asn	Phe	Ser	Ile	Leu
			85						90					95	
Tyr	Trp	Leu	Gly	Asn	Gly	Ser	Phe	Ile	Glu	His	Leu	Pro	Gly	Arg	Leu
			100					105					110		
Trp	Glu	Gly	Ser	Thr	Ser	Arg	Glu	Arg	Gly	Ser	Thr	Gly	Thr	Gln	Leu
		115					120					125			
Cys	Lys	Ala	Leu	Val	Leu	Glu	Gln	Leu	Thr	Pro	Ala	Leu	His	Ser	Thr
	130					135					140				
Asn	Phe	Ser	Cys	Val	Leu	Val	Asp	Pro	Glu	Gln	Val	Val	Gln	Arg	His
145					150					155					160
Val	Val	Leu	Ala	Gln	Leu	Trp	Ala	Gly	Leu	Arg	Ala	Thr	Leu	Pro	Pro
				165					170					175	
Thr	Gln														

<210> 11  
 <211> 422  
 <212> PRT  
 <213> Homo sapiens

<400> 11

Met	Arg	His	Asn	Trp	Thr	Pro	Asp	Leu	Ser	Pro	Leu	Trp	Val	Leu	Leu
1			5					10						15	
Leu	Cys	Ala	His	Val	Val	Thr	Leu	Leu	Val	Arg	Ala	Thr	Pro	Val	Ser
			20				25						30		
Gln	Thr	Thr	Thr	Ala	Ala	Thr	Ala	Ser	Val	Arg	Ser	Thr	Lys	Asp	Pro

35					40					45					
Cys	Pro	Ser	Gln	Pro	Pro	Val	Phe	Pro	Ala	Ala	Lys	Gln	Cys	Pro	Ala
50						55					60				
Leu	Glu	Val	Thr	Trp	Pro	Glu	Val	Glu	Val	Pro	Leu	Asn	Gly	Thr	Leu
65					70					75					80
Ser	Leu	Ser	Cys	Val	Ala	Cys	Ser	Arg	Phe	Pro	Asn	Phe	Ser	Ile	Leu
				85					90					95	
Tyr	Trp	Leu	Gly	Asn	Gly	Ser	Phe	Ile	Glu	His	Leu	Pro	Gly	Arg	Leu
			100					105					110		
Trp	Glu	Gly	Ser	Thr	Ser	Arg	Glu	Arg	Gly	Ser	Thr	Gly	Thr	Gln	Leu
		115					120					125			
Cys	Lys	Ala	Leu	Val	Leu	Glu	Gln	Leu	Thr	Pro	Ala	Leu	His	Ser	Thr
130						135					140				
Asn	Phe	Ser	Cys	Val	Leu	Val	Asp	Pro	Glu	Gln	Val	Val	Gln	Arg	His
145					150					155					160
Val	Val	Leu	Ala	Gln	Leu	Trp	Ala	Gly	Leu	Arg	Ala	Thr	Leu	Pro	Pro
				165					170					175	
Thr	Gln	Glu	Ala	Leu	Pro	Ser	Ser	His	Ser	Ser	Pro	Gln	Gln	Gln	Gly
			180					185					190		
Arg	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu
		195					200					205			
Ala	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp
210						215					220				
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp
225					230					235					240
Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly
				245					250					255	
Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn
			260					265					270		
Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp
		275					280					285			
Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro
290						295					300				
Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu
305					310					315					320
Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn
				325					330					335	
Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile
			340					345					350		
Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr
		355					360					365			

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
 370 375 380  
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
 385 390 395 400  
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
 405 410 415  
 Ser Leu Ser Pro Gly Lys  
 420

<210> 12  
 <211> 579  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (1)..(579)

<220>  
 <221> sig\_peptide  
 <222> (1)..(108)

<220>  
 <221> mat\_peptide  
 <222> (109)..()

<400> 12  
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 Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val Ala Met  
 -35 -30 -25  
 aaa ttt att gac aat acg ctt tac ttt ata gct gaa gat gat gaa aac 96  
 Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala Glu Asp Asp Glu Asn  
 -20 -15 -10 -5  
 ctg gaa tca gat tac ttt ggc aag ctt gaa tct aaa tta tca gtc ata 144  
 Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile  
 -1 1 5 10  
 aga aat ttg aat gac caa gtt ctc ttc att gac caa gga aat cgg cct 192  
 Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro  
 15 20 25  
 cta ttt gaa gat atg act gat tct gac tgt aga gat aat gca ccc cgg 240  
 Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg  
 30 35 40  
 acc ata ttt att ata agt atg tat aaa gat agc cag cct aga ggt atg 288  
 Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met  
 45 50 55 60  
 gct gta act atc tct gtg aag tgt gag aaa att tca ayt ctc tcc tgt 336  
 Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys  
 65 70 75

gag aac aaa att att tcc ttt aag gaa atg aat cct cct gat aac atc	384
Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile	
80 85 90	
aag gat aca aaa agt gac atc ata ttc ttt cag aga agt gtc cca gga	432
Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly	
95 100 105	
cat gat aat aag atg caa ttt gaa tct tca tca tac gaa gga tac ttt	480
His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe	
110 115 120	
cta gct tgt gaa aaa gag aga gac ctt ttt aaa ctc att ttg aaa aaa	528
Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys	
125 130 135 140	
gag gat gaa ttg ggg gat aga tct ata atg ttc act gtt caa aac gaa	576
Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu	
145 150 155	
gac	579
Asp	

<210> 13  
 <211> 193  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (73)..(73)  
 <223> The 'Xaa' at location 73 stands for Thr, or Ile.

<400> 13

Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val Ala Met	
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Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala Glu Asp Asp Glu Asn	
-20 -15 -10 -5	
Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile	
-1 1 5 10	
Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro	
15 20 25	
Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg	
30 35 40	
Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met	
45 50 55 60	
Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys	
65 70 75	
Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile	
80 85 90	



Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly  
 95 100 105  
 His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe  
 110 115 120  
 Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys  
 125 130 135 140  
 Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu  
 145 150 155

Asp

<210> 14  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

<400> 14

Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn  
 1 5 10 15  
 Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp  
 20 25 30  
 Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile  
 35 40 45  
 Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile  
 50 55 60  
 Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn Lys Ile  
 65 70 75 80  
 Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys  
 85 90 95  
 Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys  
 100 105 110  
 Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu  
 115 120 125  
 Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu  
 130 135 140  
 Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp  
 145 150 155

<210> 15  
 <211> 765  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> CDS  
 <222> (4)..(765)

<400> 15

gtc atg gaa tac gcc tct gac gct tca ctg gac ccc gaa gcc ccg tgg	48
Met Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp	
1 5 10 15	
cct ccc gcg ccc cgc gct cgc gcc tgc cgc gta ctg cct tgg gcc ctg	96
Pro Pro Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu	
20 25 30	
gtc gcg ggg ctg ctg ctg ctg ctg ctg ctc gct gcc gcc tgc gcc gtc	144
Val Ala Gly Leu Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val	
35 40 45	
ttc ctc gcc tgc ccc tgg gcc gtg tcc ggg gct cgc gcc tcg ccc ggc	192
Phe Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly	
50 55 60	
tcc gcg gcc agc ccg aga ctc cgc gag ggt ccc gag ctt tcg ccc gac	240
Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp	
65 70 75	
gat ccc gcc ggc ctc ttg gac ctg cgg cag ggc atg ttt gcg cag ctg	288
Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu	
80 85 90 95	
gtg gcc caa aat gtt ctg ctg atc gat ggg ccc ctg agc tgg tac agt	336
Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser	
100 105 110	
gac cca ggc ctg gca ggc gtg tcc ctg acg ggg ggc ctg agc tac aaa	384
Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys	
115 120 125	
gag gac acg aag gag ctg gtg gtg gcc aag gct gga gtc tac tat gtc	432
Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val	
130 135 140	
ttc ttt caa cta gag ctg cgg cgc gtg gtg gcc ggc gag ggc tca ggc	480
Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly	
145 150 155	
tcc gtt tca ctt gcg ctg cac ctg cag cca ctg cgc tct gct gct ggg	528
Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly	
160 165 170 175	
gcc gcc gcc ctg gct ttg acc gtg gac ctg cca ccc gcc tcc tcc gag	576
Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu	
180 185 190	
gct cgg aac tcg gcc ttc ggt ttc cag ggc cgc ttg ctg cac ctg agt	624
Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser	
195 200 205	
gcc ggc cag cgc ctg ggc gtc cat ctt cac act gag gcc agg gca cgc	672
Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg	
210 215 220	
cat gcc tgg cag ctt acc cag ggc gcc aca gtc ttg gga ctc ttc cgg	720

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg  
 225 230 235

gtg acc ccc gaa atc cca gcc gga ctc cct tca ccg agg tcg gaa  
 Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu  
 240 245 250

765

<210> 16  
 <211> 254  
 <212> PRT  
 <213> Homo sapiens

<400> 16

Met Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro  
 1 5 10 15

Pro Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu Val  
 20 25 30

Ala Gly Leu Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe  
 35 40 45

Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser  
 50 55 60

Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp  
 65 70 75 80

Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val  
 85 90 95

Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp  
 100 105 110

Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu  
 115 120 125

Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe  
 130 135 140

Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser  
 145 150 155 160

Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala  
 165 170 175

Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala  
 180 185 190

Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala  
 195 200 205

Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His  
 210 215 220

Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val  
 225 230 235 240

Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu

<210> 17  
 <211> 1415  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (120)..(884)

<220>  
 <221> sig\_peptide  
 <222> (120)..(189)

<220>  
 <221> mat\_peptide  
 <222> (189)..()

<400> 17  
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 ttgattaaaa ttctcttggga atcagcttttg ctagtatcat acctgtgcca gatttcata 119  
 atg gga aac agc tgt tac aac ata gta gcc act ctg ttg ctg gtc ctc 167  
 Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu  
 -20 -15 -10  
 aac ttt gag agg aca aga tca ttg cag gat cct tgt agt aac tgc cca 215  
 Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro  
 -5 -1 1 5  
 gct ggt aca ttc tgt gat aat aac agg aat cag att tgc agt ccc tgt 263  
 Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys  
 10 15 20 25  
 cct cca aat agt ttc tcc agc gca ggt gga caa agg acc tgt gac ata 311  
 Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile  
 30 35 40  
 tgc agg cag tgt aaa ggt gtt ttc agg acc agg aag gag tgt tcc tcc 359  
 Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser  
 45 50 55  
 acc agc aat gca gag tgt gac tgc act cca ggg ttt cac tgc ctg ggg 407  
 Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly  
 60 65 70  
 gca gga tgc agc atg tgt gaa cag gat tgt aaa caa ggt caa gaa ctg 455  
 Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu  
 75 80 85  
 aca aaa aaa ggt tgt aaa gac tgt tgc ttt ggg aca ttt aac gat cag 503  
 Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln  
 90 95 100 105  
 aaa cgt ggc atc tgt cga ccc tgg aca aac tgt tct ttg gat gga aag 551  
 Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys  
 110 115 120

tct gtg ctt gtg aat ggg acg aag gag agg gac gtg gtc tgt gga cca	599
Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro	
125 130 135	
tct cca gcc gac ctc tct ccg gga gca tcc tct gtg acc ccg cct gcc	647
Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala	
140 145 150	
cct gcg aga gag cca gga cac tct ccg cag atc atc tcc ttc ttt ctt	695
Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu	
155 160 165	
gcg ctg acg tgc act gcg ttg ctc ttc ctg ctg ttc ttc ctc acg ctc	743
Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu	
170 175 180 185	
cgt ttc tct gtt gtt aaa cgg ggc aga aag aaa ctc ctg tat ata ttc	791
Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe	
190 195 200	
aaa caa cca ttt atg aga cca gta caa act act caa gag gaa gat ggc	839
Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly	
205 210 215	
tgt agc tgc cga ttt cca gaa gaa gaa gaa gga gga tgt gaa ctg	884
Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu	
220 225 230	
tgaaatggaa gtcaataggg ctggtgggac tttcttgaaa agaagcaagg aaatatgagt	944
catccgctat cacagctttc aaaagcaaga acaccatcct acataatacc caggattccc	1004
ccaacacacg ttctttttcta aatgccaatg agttggcctt taaaaatgca ccactttttt	1064
tttttttttt gacaggggtct cactctgtca ccagggttg agtgcagtgg caccaccatg	1124
gctctctgca gccttgacct ctggggagctc aagtgatcct cctgcctcag tctcctagta	1184
gctggaacta caaggaaggg ccaccacacc tgactaactt ttttgttttt tgtttggtaa	1244
agatggcatt tcgccatggt gtacaggctg gtctcaaaact cctaggttca ctttggcctc	1304
ccaaagtgct gggattacag acatgaactg ccaggcccgg ccaaaataat gcaccacttt	1364
taacagaaca gacagatgag gacagagctg gtgataaaaa aaaaaaaaaa a	1415

<210> 18  
 <211> 255  
 <212> PRT  
 <213> Homo sapiens

<400> 18

Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu
-20 -15 -10

Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro
-5 -1 1 5

Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys  
10 15 20 25  
Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile  
30 35 40  
Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser  
45 50 55  
Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly  
60 65 70  
Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu  
75 80 85  
Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln  
90 95 100 105  
Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys  
110 115 120  
Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro  
125 130 135  
Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala  
140 145 150  
Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu  
155 160 165  
Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu  
170 175 180 185  
Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe  
190 195 200  
Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly  
205 210 215  
Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu  
220 225 230

<210> 19  
<211> 648  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(645)

<400> 19  
atg cat gtg ccg gcg ggc tcc gtg gcc agc cac ctg ggg acc acg agc 48  
Met His Val Pro Ala Gly Ser Val Ala Ser His Leu Gly Thr Thr Ser  
1 5 10 15  
cgc agc tat ttc tat ttg acc aca gcc act ctg gct ctg tgc ctt gtc 96  
Arg Ser Tyr Phe Tyr Leu Thr Thr Ala Thr Leu Ala Leu Cys Leu Val  
20 25 30

ttc acg gtg gcc act att atg gtg ttg gtc gtt cag agg acg gac tcc	144
Phe Thr Val Ala Thr Ile Met Val Leu Val Val Gln Arg Thr Asp Ser	
35 40 45	
att ccc aac tca cct gac aac gtc ccc ctc aaa gga gga aat tgc tca	192
Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys Gly Gly Asn Cys Ser	
50 55 60	
gaa gac ctc tta tgt atc ctg aaa aga gct cca ttc aag aag tca tgg	240
Glu Asp Leu Leu Cys Ile Leu Lys Arg Ala Pro Phe Lys Lys Ser Trp	
65 70 75 80	
gcc tac ctc caa gtg gca aag cat cta aac aaa acc aag ttg tct tgg	288
Ala Tyr Leu Gln Val Ala Lys His Leu Asn Lys Thr Lys Leu Ser Trp	
85 90 95	
aac aaa gat ggc att ctc cat gga gtc aga tat cag gat ggg aat ctg	336
Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr Gln Asp Gly Asn Leu	
100 105 110	
gtg atc caa ttc cct ggt ttg tac ttc atc att tgc caa ctg cag ttt	384
Val Ile Gln Phe Pro Gly Leu Tyr Phe Ile Ile Cys Gln Leu Gln Phe	
115 120 125	
ctt gta caa tgc cca aat aat tct gtc gat ctg aag ttg gag ctt ctc	432
Leu Val Gln Cys Pro Asn Asn Ser Val Asp Leu Lys Leu Glu Leu Leu	
130 135 140	
atc aac aag cat atc aaa aaa cag gcc ctg gtg aca gtg tgt gag tct	480
Ile Asn Lys His Ile Lys Lys Gln Ala Leu Val Thr Val Cys Glu Ser	
145 150 155 160	
gga atg caa acg aaa cac gta tac cag aat ctc tct caa ttc ttg ctg	528
Gly Met Gln Thr Lys His Val Tyr Gln Asn Leu Ser Gln Phe Leu Leu	
165 170 175	
gat tac ctg cag gtc aac acc acc ata tca gtc aat gtg gat aca ttc	576
Asp Tyr Leu Gln Val Asn Thr Thr Ile Ser Val Asn Val Asp Thr Phe	
180 185 190	
cag tac ata gat aca agc acc ttt cct ctt gag aat gtg ttg tcc atc	624
Gln Tyr Ile Asp Thr Ser Thr Phe Pro Leu Glu Asn Val Leu Ser Ile	
195 200 205	
ttc tta tac agt aat tca gac tga	648
Phe Leu Tyr Ser Asn Ser Asp	
210 215	

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 <213> Homo sapiens

<400> 20

Met His Val Pro Ala Gly Ser Val Ala Ser His Leu Gly Thr Thr Ser
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Arg Ser Tyr Phe Tyr Leu Thr Thr Ala Thr Leu Ala Leu Cys Leu Val

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Phe	Thr	Val	Ala	Thr	Ile	Met	Val	Leu	Val	Val	Gln	Arg	Thr	Asp	Ser	
35					40					45						
Ile	Pro	Asn	Ser	Pro	Asp	Asn	Val	Pro	Leu	Lys	Gly	Gly	Asn	Cys	Ser	
50					55					60						
Glu	Asp	Leu	Leu	Cys	Ile	Leu	Lys	Arg	Ala	Pro	Phe	Lys	Lys	Ser	Trp	
65					70					75					80	
Ala	Tyr	Leu	Gln	Val	Ala	Lys	His	Leu	Asn	Lys	Thr	Lys	Leu	Ser	Trp	
85					90					95						
Asn	Lys	Asp	Gly	Ile	Leu	His	Gly	Val	Arg	Tyr	Gln	Asp	Gly	Asn	Leu	
100					105					110						
Val	Ile	Gln	Phe	Pro	Gly	Leu	Tyr	Phe	Ile	Ile	Cys	Gln	Leu	Gln	Phe	
115					120					125						
Leu	Val	Gln	Cys	Pro	Asn	Asn	Ser	Val	Asp	Leu	Lys	Leu	Glu	Leu	Leu	
130					135					140						
Ile	Asn	Lys	His	Ile	Lys	Lys	Gln	Ala	Leu	Val	Thr	Val	Cys	Glu	Ser	
145					150					155					160	
Gly	Met	Gln	Thr	Lys	His	Val	Tyr	Gln	Asn	Leu	Ser	Gln	Phe	Leu	Leu	
165					170					175						
Asp	Tyr	Leu	Gln	Val	Asn	Thr	Thr	Ile	Ser	Val	Asn	Val	Asp	Thr	Phe	
180					185					190						
Gln	Tyr	Ile	Asp	Thr	Ser	Thr	Phe	Pro	Leu	Glu	Asn	Val	Leu	Ser	Ile	
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Phe	Leu	Tyr	Ser	Asn	Ser	Asp										
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 <212> DNA  
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 <222> (1)..(702)

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Met	Asp	Pro	Gly	Leu	Gln	Gln	Ala	Leu	Asn	Gly	Met	Ala	Pro	Pro	Gly					
1				5				10					15							
gac aca gcc atg cat gtg ccg gcg ggc tcc gtg gcc agc cac ctg ggg																				96
Asp	Thr	Ala	Met	His	Val	Pro	Ala	Gly	Ser	Val	Ala	Ser	His	Leu	Gly					
			20					25					30							
acc acg agc cgc agc tat ttc tat ttg acc aca gcc act ctg gct ctg																				144
Thr	Thr	Ser	Arg	Ser	Tyr	Phe	Tyr	Leu	Thr	Thr	Ala	Thr	Leu	Ala	Leu					
			35				40						45							



tgc ctt gtc ttc acg gtg gcc act att atg gtg ttg gtc gtt cag agg	192
Cys Leu Val Phe Thr Val Ala Thr Ile Met Val Leu Val Val Gln Arg	
50 55 60	
acg gac tcc att ccc aac tca cct gac aac gtc ccc ctc aaa gga gga	240
Thr Asp Ser Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys Gly Gly	
65 70 75 80	
aat tgc tca gaa gac ctc tta tgt atc ctg aaa aga gct cca ttc aag	288
Asn Cys Ser Glu Asp Leu Leu Cys Ile Leu Lys Arg Ala Pro Phe Lys	
85 90 95	
aag tca tgg gcc tac ctc caa gtg gca aag cat cta aac aaa acc aag	336
Lys Ser Trp Ala Tyr Leu Gln Val Ala Lys His Leu Asn Lys Thr Lys	
100 105 110	
ttg tct tgg aac aaa gat ggc att ctc cat gga gtc aga tat cag gat	384
Leu Ser Trp Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr Gln Asp	
115 120 125	
ggg aat ctg gtg atc caa ttc cct ggt ttg tac ttc atc att tgc caa	432
Gly Asn Leu Val Ile Gln Phe Pro Gly Leu Tyr Phe Ile Ile Cys Gln	
130 135 140	
ctg cag ttt ctt gta caa tgc cca aat aat tct gtc gat ctg aag ttg	480
Leu Gln Phe Leu Val Gln Cys Pro Asn Asn Ser Val Asp Leu Lys Leu	
145 150 155 160	
gag ctt ctc atc aac aag cat atc aaa aaa cag gcc ctg gtg aca gtg	528
Glu Leu Leu Ile Asn Lys His Ile Lys Lys Gln Ala Leu Val Thr Val	
165 170 175	
tgt gag tct gga atg caa acg aaa cac gta tac cag aat ctc tct caa	576
Cys Glu Ser Gly Met Gln Thr Lys His Val Tyr Gln Asn Leu Ser Gln	
180 185 190	
ttc ttg ctg gat tac ctg cag gtc aac acc acc ata tca gtc aat gtg	624
Phe Leu Leu Asp Tyr Leu Gln Val Asn Thr Thr Ile Ser Val Asn Val	
195 200 205	
gat aca ttc cag tac ata gat aca agc acc ttt cct ctt gag aat gtg	672
Asp Thr Phe Gln Tyr Ile Asp Thr Ser Thr Phe Pro Leu Glu Asn Val	
210 215 220	
ttg tcc atc ttc tta tac agt aat tca gac tga	705
Leu Ser Ile Phe Leu Tyr Ser Asn Ser Asp	
225 230	

<210> 22  
 <211> 234  
 <212> PRT  
 <213> Homo sapiens

<400> 22

Met Asp Pro Gly Leu Gln Gln Ala Leu Asn Gly Met Ala Pro Pro Gly
1 5 10 15

Asp Thr Ala Met His Val Pro Ala Gly Ser Val Ala Ser His Leu Gly

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Thr	Thr	Ser	Arg	Ser	Tyr	Phe	Tyr	Leu	Thr	Thr	Ala	Thr	Leu	Ala	Leu
		35					40					45			
Cys	Leu	Val	Phe	Thr	Val	Ala	Thr	Ile	Met	Val	Leu	Val	Val	Gln	Arg
	50					55					60				
Thr	Asp	Ser	Ile	Pro	Asn	Ser	Pro	Asp	Asn	Val	Pro	Leu	Lys	Gly	Gly
65					70					75					80
Asn	Cys	Ser	Glu	Asp	Leu	Leu	Cys	Ile	Leu	Lys	Arg	Ala	Pro	Phe	Lys
				85					90					95	
Lys	Ser	Trp	Ala	Tyr	Leu	Gln	Val	Ala	Lys	His	Leu	Asn	Lys	Thr	Lys
			100					105					110		
Leu	Ser	Trp	Asn	Lys	Asp	Gly	Ile	Leu	His	Gly	Val	Arg	Tyr	Gln	Asp
		115					120					125			
Gly	Asn	Leu	Val	Ile	Gln	Phe	Pro	Gly	Leu	Tyr	Phe	Ile	Ile	Cys	Gln
	130					135					140				
Leu	Gln	Phe	Leu	Val	Gln	Cys	Pro	Asn	Asn	Ser	Val	Asp	Leu	Lys	Leu
145					150					155					160
Glu	Leu	Leu	Ile	Asn	Lys	His	Ile	Lys	Lys	Gln	Ala	Leu	Val	Thr	Val
				165					170					175	
Cys	Glu	Ser	Gly	Met	Gln	Thr	Lys	His	Val	Tyr	Gln	Asn	Leu	Ser	Gln
			180					185					190		
Phe	Leu	Leu	Asp	Tyr	Leu	Gln	Val	Asn	Thr	Thr	Ile	Ser	Val	Asn	Val
		195					200					205			
Asp	Thr	Phe	Gln	Tyr	Ile	Asp	Thr	Ser	Thr	Phe	Pro	Leu	Glu	Asn	Val
	210					215					220				
Leu	Ser	Ile	Phe	Leu	Tyr	Ser	Asn	Ser	Asp						
225					230										

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Met	Arg	Val	Leu	Leu	Ala	Ala	Leu	Gly	Leu	Leu	Phe	Leu	Gly	Ala	Leu	
1				5					10					15		
cga	gcc	ttc	cca	cag	gat	cga	ccc	ttc	gag	gac	acc	tgt	cat	gga	aac	96
Arg	Ala	Phe	Pro	Gln	Asp	Arg	Pro	Phe	Glu	Asp	Thr	Cys	His	Gly	Asn	
			20					25					30			

ccc agc cac tac tat gac aag gct gtc agg agg tgc tgt tac cgc tgc Pro Ser His Tyr Tyr Asp Lys Ala Val Arg Arg Cys Cys Tyr Arg Cys 35 40 45	144
ccc atg ggg ctg ttc ccg aca cag cag tgc cca cag agg cct act gac Pro Met Gly Leu Phe Pro Thr Gln Gln Cys Pro Gln Arg Pro Thr Asp 50 55 60	192
tgc agg aag cag tgt gag cct gac tac tac ctg gat gag gcc gac cgc Cys Arg Lys Gln Cys Glu Pro Asp Tyr Tyr Leu Asp Glu Ala Asp Arg 65 70 75 80	240
tgt aca gcc tgc gtg act tgt tct cga gat gac ctc gtg gag aag acg Cys Thr Ala Cys Val Thr Cys Ser Arg Asp Asp Leu Val Glu Lys Thr 85 90 95	288
ccg tgt gca tgg aac tcc tcc cgt gtc tgc gaa tgt cga ccc ggc atg Pro Cys Ala Trp Asn Ser Ser Arg Val Cys Glu Cys Arg Pro Gly Met 100 105 110	336
ttc tgt tcc acg tct gcc gtc aac tcc tgt gcc cgc tgc ttc ttc cat Phe Cys Ser Thr Ser Ala Val Asn Ser Cys Ala Arg Cys Phe Phe His 115 120 125	384
tct gtc tgt ccg gca ggg atg att gtc aag ttc cca ggc acg gcg cag Ser Val Cys Pro Ala Gly Met Ile Val Lys Phe Pro Gly Thr Ala Gln 130 135 140	432
aag aac acg gtc tgt gag ccg gct tcc cca ggg gtc agc cct gcc tgt Lys Asn Thr Val Cys Glu Pro Ala Ser Pro Gly Val Ser Pro Ala Cys 145 150 155 160	480
gcc agc cca gag aac tgc aag gaa ccc tcc agt ggc acc atc ccc cag Ala Ser Pro Glu Asn Cys Lys Glu Pro Ser Ser Gly Thr Ile Pro Gln 165 170 175	528
gcc aag ccc acc ccg gtg tcc cca gca acc tcc agt gcc agc acc atg Ala Lys Pro Thr Pro Val Ser Pro Ala Thr Ser Ser Ala Ser Thr Met 180 185 190	576
cct gta aga ggg ggc acc cgc ctc gcc cag gaa gct gct tct aaa ctg Pro Val Arg Gly Gly Thr Arg Leu Ala Gln Glu Ala Ala Ser Lys Leu 195 200 205	624
acg agg gct ccc gac tct ccc tcc tct gtg gga agg cct agt tca gat Thr Arg Ala Pro Asp Ser Pro Ser Ser Val Gly Arg Pro Ser Ser Asp 210 215 220	672
cca ggt ctg tcc cca aca cag cca tgc cca gag ggg tct ggt gat tgc Pro Gly Leu Ser Pro Thr Gln Pro Cys Pro Glu Gly Ser Gly Asp Cys 225 230 235 240	720
aga aag cag tgt gag ccc gac tac tac ctg gac gag gcc ggc cgc tgc Arg Lys Gln Cys Glu Pro Asp Tyr Tyr Leu Asp Glu Ala Gly Arg Cys 245 250 255	768
aca gcc tgc gtg agc tgt tct cga gat gac ctt gtg gag aag acg cca Thr Ala Cys Val Ser Cys Ser Arg Asp Asp Leu Val Glu Lys Thr Pro 260 265 270	816
tgt gca tgg aac tcc tcc cgc acc tgc gaa tgt cga cct ggc atg atc	864

Cys	Ala	Trp	Asn	Ser	Ser	Arg	Thr	Cys	Glu	Cys	Arg	Pro	Gly	Met	Ile		
	275						280					285					
tgt	gcc	aca	tca	gcc	acc	aac	tcc	tgt	gcc	cgc	tgt	gtc	ccc	tac	cca		912
Cys	Ala	Thr	Ser	Ala	Thr	Asn	Ser	Cys	Ala	Arg	Cys	Val	Pro	Tyr	Pro		
	290					295					300						
atc	tgt	gca	gga	gag	acg	gtc	acc	aag	ccc	cag	gat	atg	gct	gag	aag		960
Ile	Cys	Ala	Gly	Glu	Thr	Val	Thr	Lys	Pro	Gln	Asp	Met	Ala	Glu	Lys		
305					310					315					320		
gac	acc	acc	ttt	gag	gcg	cca	ccc	ctg	ggg	acc	cag	ccg	gac	tgc	aac		1008
Asp	Thr	Thr	Phe	Glu	Ala	Pro	Pro	Leu	Gly	Thr	Gln	Pro	Asp	Cys	Asn		
				325					330					335			
ccc	acc	cca	gag	aat	ggc	gag	gcg	cct	gcc	agc	acc	agc	ccc	act	cag		1056
Pro	Thr	Pro	Glu	Asn	Gly	Glu	Ala	Pro	Ala	Ser	Thr	Ser	Pro	Thr	Gln		
			340					345					350				
agc	ttg	ctg	gtg	gac	tcc	cag	gcc	agt	aag	acg	ctg	ccc	atc	cca	acc		1104
Ser	Leu	Leu	Val	Asp	Ser	Gln	Ala	Ser	Lys	Thr	Leu	Pro	Ile	Pro	Thr		
	355					360						365					
agc	gct	ccc	gtc	gct	ctc	tcc	tcc	acg	ggg	aag	ccc	gtt	ctg	gat	gca		1152
Ser	Ala	Pro	Val	Ala	Leu	Ser	Ser	Thr	Gly	Lys	Pro	Val	Leu	Asp	Ala		
	370					375					380						
ggg	cca	gtg	ctc	ttc	tgg	gtg	atc	ctg	gtg	ttg	gtt	gtg	gtg	gtc	ggc		1200
Gly	Pro	Val	Leu	Phe	Trp	Val	Ile	Leu	Val	Leu	Val	Val	Val	Val	Gly		
385					390					395					400		
tcc	agc	gcc	ttc	ctc	ctg	tgc	cac	cgg	agg	gcc	tgc	agg	aag	cga	att		1248
Ser	Ser	Ala	Phe	Leu	Leu	Cys	His	Arg	Arg	Ala	Cys	Arg	Lys	Arg	Ile		
				405					410					415			
cgg	cag	aag	ctc	cac	ctg	tgc	tac	ccg	gtc	cag	acc	tcc	cag	ccc	aag		1296
Arg	Gln	Lys	Leu	His	Leu	Cys	Tyr	Pro	Val	Gln	Thr	Ser	Gln	Pro	Lys		
			420					425					430				
cta	gag	ctt	gtg	gat	tcc	aga	ccc	agg	agg	agc	tca	acg	cag	ctg	agg		1344
Leu	Glu	Leu	Val	Asp	Ser	Arg	Pro	Arg	Arg	Ser	Ser	Thr	Gln	Leu	Arg		
		435					440					445					
agt	ggt	gcg	tcg	gtg	aca	gaa	ccc	gtc	gcg	gaa	gag	cga	ggg	tta	atg		1392
Ser	Gly	Ala	Ser	Val	Thr	Glu	Pro	Val	Ala	Glu	Glu	Arg	Gly	Leu	Met		
	450					455					460						
agc	cag	cca	ctg	atg	gag	acc	tgc	cac	agc	gtg	ggg	gca	gcc	tac	ctg		1440
Ser	Gln	Pro	Leu	Met	Glu	Thr	Cys	His	Ser	Val	Gly	Ala	Ala	Tyr	Leu		
465					470					475					480		
gag	agc	ctg	ccg	ctg	cag	gat	gcc	agc	ccg	gcc	ggg	ggc	ccc	tcg	tcc		1488
Glu	Ser	Leu	Pro	Leu	Gln	Asp	Ala	Ser	Pro	Ala	Gly	Gly	Pro	Ser	Ser		
				485					490					495			
ccc	agg	gac	ctt	cct	gag	ccc	cgg	gtg	tcc	acg	gag	cac	acc	aat	aac		1536
Pro	Arg	Asp	Leu	Pro	Glu	Pro	Arg	Val	Ser	Thr	Glu	His	Thr	Asn	Asn		
			500					505					510				
aag	att	gag	aaa	atc	tac	atc	atg	aag	gct	gac	acc	gtg	atc	gtg	ggg		1584
Lys	Ile	Glu	Lys	Ile	Tyr	Ile	Met	Lys	Ala	Asp	Thr	Val	Ile	Val	Gly		

515	520	525	
acc gtg aag gct gag ctg ccg gag ggc cgg ggc ctg gcg ggg cca gca			1632
Thr Val Lys Ala Glu Leu Pro Glu Gly Arg Gly Leu Ala Gly Pro Ala			
530	535	540	
gag ccc gag ttg gag gag gag ctg gag gcg gac cat acc ccc cac tac			1680
Glu Pro Glu Leu Glu Glu Glu Leu Glu Ala Asp His Thr Pro His Tyr			
545	550	555	560
ccc gag cag gag aca gaa ccg cct ctg ggc agc tgc agc gat gtc atg			1728
Pro Glu Gln Glu Thr Glu Pro Pro Leu Gly Ser Cys Ser Asp Val Met			
	565	570	575
ctc tca gtg gaa gag gaa ggg aaa gaa gac ccc ttg ccc aca gct gcc			1776
Leu Ser Val Glu Glu Glu Gly Lys Glu Asp Pro Leu Pro Thr Ala Ala			
	580	585	590
tct gga aag tga			1788
Ser Gly Lys			
595			
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Met Arg Val Leu Leu Ala Ala Leu Gly Leu Leu Phe Leu Gly Ala Leu			
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Arg Ala Phe Pro Gln Asp Arg Pro Phe Glu Asp Thr Cys His Gly Asn			
	20	25	30
Pro Ser His Tyr Tyr Asp Lys Ala Val Arg Arg Cys Cys Tyr Arg Cys			
	35	40	45
Pro Met Gly Leu Phe Pro Thr Gln Gln Cys Pro Gln Arg Pro Thr Asp			
	50	55	60
Cys Arg Lys Gln Cys Glu Pro Asp Tyr Tyr Leu Asp Glu Ala Asp Arg			
65	70	75	80
Cys Thr Ala Cys Val Thr Cys Ser Arg Asp Asp Leu Val Glu Lys Thr			
	85	90	95
Pro Cys Ala Trp Asn Ser Ser Arg Val Cys Glu Cys Arg Pro Gly Met			
	100	105	110
Phe Cys Ser Thr Ser Ala Val Asn Ser Cys Ala Arg Cys Phe Phe His			
	115	120	125
Ser Val Cys Pro Ala Gly Met Ile Val Lys Phe Pro Gly Thr Ala Gln			
	130	135	140
Lys Asn Thr Val Cys Glu Pro Ala Ser Pro Gly Val Ser Pro Ala Cys			
145	150	155	160
Ala Ser Pro Glu Asn Cys Lys Glu Pro Ser Ser Gly Thr Ile Pro Gln			

165					170					175					
Ala	Lys	Pro	Thr	Pro	Val	Ser	Pro	Ala	Thr	Ser	Ser	Ala	Ser	Thr	Met
			180					185					190		
Pro	Val	Arg	Gly	Gly	Thr	Arg	Leu	Ala	Gln	Glu	Ala	Ala	Ser	Lys	Leu
		195					200					205			
Thr	Arg	Ala	Pro	Asp	Ser	Pro	Ser	Ser	Val	Gly	Arg	Pro	Ser	Ser	Asp
	210					215					220				
Pro	Gly	Leu	Ser	Pro	Thr	Gln	Pro	Cys	Pro	Glu	Gly	Ser	Gly	Asp	Cys
225					230					235					240
Arg	Lys	Gln	Cys	Glu	Pro	Asp	Tyr	Tyr	Leu	Asp	Glu	Ala	Gly	Arg	Cys
			245						250					255	
Thr	Ala	Cys	Val	Ser	Cys	Ser	Arg	Asp	Asp	Leu	Val	Glu	Lys	Thr	Pro
			260					265					270		
Cys	Ala	Trp	Asn	Ser	Ser	Arg	Thr	Cys	Glu	Cys	Arg	Pro	Gly	Met	Ile
		275					280					285			
Cys	Ala	Thr	Ser	Ala	Thr	Asn	Ser	Cys	Ala	Arg	Cys	Val	Pro	Tyr	Pro
		290				295					300				
Ile	Cys	Ala	Gly	Glu	Thr	Val	Thr	Lys	Pro	Gln	Asp	Met	Ala	Glu	Lys
305					310					315					320
Asp	Thr	Thr	Phe	Glu	Ala	Pro	Pro	Leu	Gly	Thr	Gln	Pro	Asp	Cys	Asn
			325						330					335	
Pro	Thr	Pro	Glu	Asn	Gly	Glu	Ala	Pro	Ala	Ser	Thr	Ser	Pro	Thr	Gln
			340					345					350		
Ser	Leu	Leu	Val	Asp	Ser	Gln	Ala	Ser	Lys	Thr	Leu	Pro	Ile	Pro	Thr
		355					360					365			
Ser	Ala	Pro	Val	Ala	Leu	Ser	Ser	Thr	Gly	Lys	Pro	Val	Leu	Asp	Ala
		370				375					380				
Gly	Pro	Val	Leu	Phe	Trp	Val	Ile	Leu	Val	Leu	Val	Val	Val	Val	Gly
385					390					395					400
Ser	Ser	Ala	Phe	Leu	Leu	Cys	His	Arg	Arg	Ala	Cys	Arg	Lys	Arg	Ile
			405					410					415		
Arg	Gln	Lys	Leu	His	Leu	Cys	Tyr	Pro	Val	Gln	Thr	Ser	Gln	Pro	Lys
			420					425					430		
Leu	Glu	Leu	Val	Asp	Ser	Arg	Pro	Arg	Arg	Ser	Ser	Thr	Gln	Leu	Arg
		435					440					445			
Ser	Gly	Ala	Ser	Val	Thr	Glu	Pro	Val	Ala	Glu	Glu	Arg	Gly	Leu	Met
		450				455					460				
Ser	Gln	Pro	Leu	Met	Glu	Thr	Cys	His	Ser	Val	Gly	Ala	Ala	Tyr	Leu
465					470					475					480
Glu	Ser	Leu	Pro	Leu	Gln	Asp	Ala	Ser	Pro	Ala	Gly	Gly	Pro	Ser	Ser
			485						490					495	

Pro Arg Asp Leu Pro Glu Pro Arg Val Ser Thr Glu His Thr Asn Asn  
500 505 510

Lys Ile Glu Lys Ile Tyr Ile Met Lys Ala Asp Thr Val Ile Val Gly  
515 520 525

Thr Val Lys Ala Glu Leu Pro Glu Gly Arg Gly Leu Ala Gly Pro Ala  
530 535 540

Glu Pro Glu Leu Glu Glu Glu Leu Glu Ala Asp His Thr Pro His Tyr  
545 550 555 560

Pro Glu Gln Glu Thr Glu Pro Pro Leu Gly Ser Cys Ser Asp Val Met  
565 570 575

Leu Ser Val Glu Glu Glu Gly Lys Glu Asp Pro Leu Pro Thr Ala Ala  
580 585 590

Ser Gly Lys  
595

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<212> DNA  
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<222> (138)..(686)

<400> 25  
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tttctgggga aaacttcagt tttatcgac gttccccttt tccatatctt catcttcctt 120

ctaccagat tgtgaag atg gaa agg gtc caa ccc ctg gaa gag aat gtg 170  
Met Glu Arg Val Gln Pro Leu Glu Glu Asn Val  
1 5 10

gga aat gca gcc agg cca aga ttc gag agg aac aag cta ttg ctg gtg 218  
Gly Asn Ala Ala Arg Pro Arg Phe Glu Arg Asn Lys Leu Leu Leu Val  
15 20 25

gcc tct gta att cag gga ctg ggg ctg ctc ctg tgc ttc acc tac atc 266  
Ala Ser Val Ile Gln Gly Leu Gly Leu Leu Leu Cys Phe Thr Tyr Ile  
30 35 40

tgc ctg cac ttc tct gct ctt cag gta tca cat cgg tat cct cga att 314  
Cys Leu His Phe Ser Ala Leu Gln Val Ser His Arg Tyr Pro Arg Ile  
45 50 55

caa agt atc aaa gta caa ttt acc gaa tat aag aag gag aaa ggt ttc 362  
Gln Ser Ile Lys Val Gln Phe Thr Glu Tyr Lys Lys Glu Lys Gly Phe  
60 65 70 75

atc ctc act tcc caa aag gag gat gaa atc atg aag gtg cag aac aac 410  
Ile Leu Thr Ser Gln Lys Glu Asp Glu Ile Met Lys Val Gln Asn Asn  
80 85 90

tca gtc atc atc aac tgt gat ggg ttt tat ctc atc tcc ctg aag ggc	458
Ser Val Ile Ile Asn Cys Asp Gly Phe Tyr Leu Ile Ser Leu Lys Gly	
95 100 105	
tac ttc tcc cag gaa gtc aac att agc ctt cat tac cag aag gat gag	506
Tyr Phe Ser Gln Glu Val Asn Ile Ser Leu His Tyr Gln Lys Asp Glu	
110 115 120	
gag ccc ctc ttc caa ctg aag aag gtc agg tct gtc aac tcc ttg atg	554
Glu Pro Leu Phe Gln Leu Lys Lys Val Arg Ser Val Asn Ser Leu Met	
125 130 135	
gtg gcc tct ctg act tac aaa gac aaa gtc tac ttg aat gtg acc act	602
Val Ala Ser Leu Thr Tyr Lys Asp Lys Val Tyr Leu Asn Val Thr Thr	
140 145 150 155	
gac aat acc tcc ctg gat gac ttc cat gtg aat ggc gga gaa ctg att	650
Asp Asn Thr Ser Leu Asp Asp Phe His Val Asn Gly Gly Glu Leu Ile	
160 165 170	
ctt atc cat caa aat cct ggt gaa ttc tgt gtc ctt tgaggggctg	696
Leu Ile His Gln Asn Pro Gly Glu Phe Cys Val Leu	
175 180	

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 <211> 183  
 <212> PRT  
 <213> Homo sapiens

<400> 26

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Pro Arg Phe Glu Arg Asn Lys Leu Leu Leu Val Ala Ser Val Ile Gln	
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Gly Leu Gly Leu Leu Leu Cys Phe Thr Tyr Ile Cys Leu His Phe Ser	
35 40 45	
Ala Leu Gln Val Ser His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val	
50 55 60	
Gln Phe Thr Glu Tyr Lys Lys Glu Lys Gly Phe Ile Leu Thr Ser Gln	
65 70 75 80	
Lys Glu Asp Glu Ile Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn	
85 90 95	
Cys Asp Gly Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu	
100 105 110	
Val Asn Ile Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln	
115 120 125	
Leu Lys Lys Val Arg Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr	
130 135 140	
Tyr Lys Asp Lys Val Tyr Leu Asn Val Thr Thr Asp Asn Thr Ser Leu	



145                      150                      155                      160  
 Asp Asp Phe His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn  
                                  165                      170                      175  
 Pro Gly Glu Phe Cys Val Leu  
                                  180

<210> 27  
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<220>  
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                                  Met Cys Val Gly Ala Arg Arg Leu Gly Arg Gly Pro  
                                  1                      5                      10  
 tgt gcg gct ctg ctc ctc ctg ggc ctg ggg ctg agc acc gtg acg ggg 98  
 Cys Ala Ala Leu Leu Leu Leu Gly Leu Gly Leu Ser Thr Val Thr Gly  
                                  15                      20                      25  
 ctc cac tgt gtc ggg gac acc tac ccc agc aac gac cgg tgc tgc cac 146  
 Leu His Cys Val Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His  
                                  30                      35                      40  
 gag tgc agg cca ggc aac ggg atg gtg agc cgc tgc agc cgc tcc cag 194  
 Glu Cys Arg Pro Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln  
                                  45                      50                      55                      60  
 aac acg gtg tgc cgt ccg tgc ggg ccg ggc ttc tac aac gac gtg gtc 242  
 Asn Thr Val Cys Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val  
                                  65                      70                      75  
 agc tcc aag ccg tgc aag ccc tgc acg tgg tgt aac ctc aga agt ggg 290  
 Ser Ser Lys Pro Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly  
                                  80                      85                      90  
 agt gag cgg aag cag ctg tgc acg gcc aca cag gac aca gtc tgc cgc 338  
 Ser Glu Arg Lys Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg  
                                  95                      100                      105  
 tgc cgg gcg ggc acc cag ccc ctg gac agc tac aag cct gga gtt gac 386  
 Cys Arg Ala Gly Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp  
                                  110                      115                      120  
 tgt gcc ccc tgc cct cca ggg cac ttc tcc cca ggc gac aac cag gcc 434  
 Cys Ala Pro Cys Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala  
                                  125                      130                      135                      140  
 tgc aag ccc tgg acc aac tgc acc ttg gct ggg aag cac acc ctg cag 482  
 Cys Lys Pro Trp Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln  
                                  145                      150                      155  
 ccg gcc agc aat agc tcg gac gca atc tgt gag gac agg gac ccc cca 530

Pro	Ala	Ser	Asn	Ser	Ser	Asp	Ala	Ile	Cys	Glu	Asp	Arg	Asp	Pro	Pro		
			160					165					170				
gcc	acg	cag	ccc	cag	gag	acc	cag	ggc	ccc	ccg	gcc	agg	ccc	atc	act		578
Ala	Thr	Gln	Pro	Gln	Glu	Thr	Gln	Gly	Pro	Pro	Ala	Arg	Pro	Ile	Thr		
		175					180					185					
gtc	cag	ccc	act	gaa	gcc	tgg	ccc	aga	acc	tca	cag	gga	ccc	tcc	acc		626
Val	Gln	Pro	Thr	Glu	Ala	Trp	Pro	Arg	Thr	Ser	Gln	Gly	Pro	Ser	Thr		
	190					195					200						
cgg	ccc	gtg	gag	gtc	ccc	ggg	ggc	cgt	gcg	gtt	gcc	gcc	atc	ctg	ggc		674
Arg	Pro	Val	Glu	Val	Pro	Gly	Gly	Arg	Ala	Val	Ala	Ala	Ile	Leu	Gly		
205					210					215					220		
ctg	ggc	ctg	gtg	ctg	ggg	ctg	ctg	ggc	ccc	ctg	gcc	atc	ctg	ctg	gcc		722
Leu	Gly	Leu	Val	Leu	Gly	Leu	Leu	Gly	Pro	Leu	Ala	Ile	Leu	Leu	Ala		
				225				230						235			
ctg	tac	ctg	ctc	cgg	agg	gac	cag	agg	ctg	ccc	ccc	gat	gcc	cac	aag		770
Leu	Tyr	Leu	Leu	Arg	Arg	Asp	Gln	Arg	Leu	Pro	Pro	Asp	Ala	His	Lys		
			240					245					250				
ccc	cct	ggg	gga	ggc	agt	ttc	cgg	acc	ccc	atc	caa	gag	gag	cag	gcc		818
Pro	Pro	Gly	Gly	Gly	Ser	Phe	Arg	Thr	Pro	Ile	Gln	Glu	Glu	Gln	Ala		
		255					260					265					
gac	gcc	cac	tcc	acc	ctg	gcc	aag	atc	tgac	ctgggc	ccaccaaggt						865
Asp	Ala	His	Ser	Thr	Leu	Ala	Lys	Ile									
	270					275											

<210> 28  
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 <213> Homo sapiens

<400> 28

Met	Cys	Val	Gly	Ala	Arg	Arg	Leu	Gly	Arg	Gly	Pro	Cys	Ala	Ala	Leu		
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Leu	Leu	Leu	Gly	Leu	Gly	Leu	Ser	Thr	Val	Thr	Gly	Leu	His	Cys	Val		
			20					25					30				
Gly	Asp	Thr	Tyr	Pro	Ser	Asn	Asp	Arg	Cys	Cys	His	Glu	Cys	Arg	Pro		
	35						40					45					
Gly	Asn	Gly	Met	Val	Ser	Arg	Cys	Ser	Arg	Ser	Gln	Asn	Thr	Val	Cys		
	50					55					60						
Arg	Pro	Cys	Gly	Pro	Gly	Phe	Tyr	Asn	Asp	Val	Val	Ser	Ser	Lys	Pro		
65					70				75						80		
Cys	Lys	Pro	Cys	Thr	Trp	Cys	Asn	Leu	Arg	Ser	Gly	Ser	Glu	Arg	Lys		
				85				90						95			
Gln	Leu	Cys	Thr	Ala	Thr	Gln	Asp	Thr	Val	Cys	Arg	Cys	Arg	Ala	Gly		
			100					105					110				
Thr	Gln	Pro	Leu	Asp	Ser	Tyr	Lys	Pro	Gly	Val	Asp	Cys	Ala	Pro	Cys		

115	120	125
Pro Pro Gly His Phe Ser	Pro Gly Asp Asn Gln	Ala Cys Lys Pro Trp
130	135	140
Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln Pro Ala Ser Asn		
145	150	155 160
Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro Ala Thr Gln Pro		
	165 170	175
Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr Val Gln Pro Thr		
	180 185	190
Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr Arg Pro Val Glu		
	195 200	205
Val Pro Gly Gly Arg Ala Val Ala Ala Ile Leu Gly Leu Gly Leu Val		
	210 215	220
Leu Gly Leu Leu Gly Pro Leu Ala Ile Leu Leu Ala Leu Tyr Leu Leu		
	225 230	235 240
Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly		
	245 250	255
Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser		
	260 265	270
Thr Leu Ala Lys Ile		
	275	

<210> 29  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (67)..(1596)

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ctactt atg gaa gat aca aag gag tct aac gtg aag aca ttt tgc tcc	108
Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser	
1 5 10	
aag aat atc cta gcc atc ctt ggc ttc tcc tct atc ata gct gtg ata	156
Lys Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile	
15 20 25 30	
gct ttg ctt gct gtg ggg ttg acc cag aac aaa gca ttg cca gaa aac	204
Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn	
35 40 45	
gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta	252
Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu	
50 55 60	

tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val 65 70 75	300
cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe 80 85 90	348
gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu 95 100 105 110	396
aga gct agg gaa gtg att cca agg tcc cag cac caa gag aca ccc gtt Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val 115 120 125	444
tac ctg gga gcc acg gca ggc atg cgg ttg ctc agg atg gaa agt gaa Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu 130 135 140	492
gag ttg gca gac agg gtt ctg gat gtg gtg gag agg agc ctc agc aac Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn 145 150 155	540
tac ccc ttt gac ttc cag ggt gcc agg atc att act ggc caa gag gaa Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu 160 165 170	588
ggg gcc tat ggc tgg att act atc aac tat ctg ctg ggc aaa ttc agt Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser 175 180 185 190	636
cag aaa aca agg tgg ttc agc ata gtc cca tat gaa acc aat aat cag Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln 195 200 205	684
gaa acc ttt gga gct ttg gac ctt ggg gga gcc tct aca caa gtc act Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr 210 215 220	732
ttt gta ccc caa aac cag act atc gag tcc cca gat aat gct ctg caa Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln 225 230 235	780
ttt cgc ctc tat ggc aag gac tac aat gtc tac aca cat agc ttc ttg Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu 240 245 250	828
tgc tat ggg aag gat cag gca ctc tgg cag aaa ctg gcc aag gac att Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile 255 260 265 270	876
cag gtt gca agt aat gaa att ctc agg gac cca tgc ttt cat cct gga Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly 275 280 285	924
tat aag aag gta gtg aac gta agt gac ctt tac aag acc ccc tgc acc Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr 290 295 300	972

aag aga ttt gag atg act ctt cca ttc cag cag ttt gaa atc cag ggt Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly 305 310 315	1020
att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn 320 325 330	1068
acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu 335 340 345 350	1116
cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val 355 360 365	1164
atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val 370 375 380	1212
act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys 385 390 395	1260
aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe 400 405 410	1308
tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr 415 420 425 430	1356
gct gat tcc tgg gag cac atc cat ttc att ggc aag atc cag ggc agc Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser 435 440 445	1404
gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile 450 455 460	1452
cca gct gag caa cca ttg tcc aca cct ctc tcc cac tcc acc tat gtc Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val 465 470 475	1500
ttc ctc atg gtt cta ttc tcc ctg gtc ctt ttc aca gtg gcc atc ata Phe Leu Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile 480 485 490	1548
ggc ttg ctt atc ttt cac aag cct tca tat ttc tgg aaa gat atg gta Gly Leu Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val 495 500 505 510	1596
tag	1599
 <210> 30 <211> 510 <212> PRT <213> Homo sapiens  <400> 30	

Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser Lys Asn  
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 Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile Ala Leu  
 20 25 30  
 Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys  
 35 40 45  
 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile  
 50 55 60  
 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln  
 65 70 75 80  
 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln  
 85 90 95  
 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala  
 100 105 110  
 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu  
 115 120 125  
 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu  
 130 135 140  
 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro  
 145 150 155 160  
 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala  
 165 170 175  
 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys  
 180 185 190  
 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr  
 195 200 205  
 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val  
 210 215 220  
 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg  
 225 230 235 240  
 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr  
 245 250 255  
 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val  
 260 265 270  
 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys  
 275 280 285  
 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg  
 290 295 300  
 Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly  
 305 310 315 320

Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser  
 325 330 335  
 Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro  
 340 345 350  
 Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys  
 355 360 365  
 Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu  
 370 375 380  
 Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser  
 385 390 395 400  
 Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly  
 405 410 415  
 Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp  
 420 425 430  
 Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala  
 435 440 445  
 Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala  
 450 455 460  
 Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu  
 465 470 475 480  
 Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu  
 485 490 495  
 Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val  
 500 505 510

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<220>  
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<400> 31

Asp Tyr Lys Asp Asp Asp Asp Lys  
 1 5

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<220>  
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<400> 32

Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser  
1 5 10

<210> 33  
<211> 13  
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<220>  
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<400> 33

Gly Ala Gly Gly Ala Gly Ser Gly Gly Gly Gly Gly Ser  
1 5 10

<210> 34  
<211> 10  
<212> PRT  
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<220>  
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<400> 34

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10

<210> 35  
<211> 9  
<212> PRT  
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<220>  
<223> peptide

<400> 35

Gly Thr Pro Gly Thr Pro Gly Thr Pro  
1 5

<210> 36  
<211> 26  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> peptide

<400> 36

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser  
20 25